

SEQUENCE LISTING

5 (1) GENERAL INFORMATION:

(i) APPLICANTS: Morrow, Casey D. and Porter, Donna, C.

10 (ii) TITLE OF INVENTION: ENCAPSIDATED RECOMBINANT POLIOVIRUS
NUCLEIC ACID AND METHODS OF MAKING AND
USING SAME

(iii) NUMBER OF SEQUENCES: 23

15 (iv) CORRESPONDENCE ADDRESS:

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(C) CITY: BOSTON
(D) STATE: MASSACHUSETTS
20 (E) COUNTRY: USA
(F) ZIP: 02109

(v) COMPUTER READABLE FORM:

25 (A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: ASCII

30 (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 000000
(B) FILING DATE: 15-FEB-1995
(C) CLASSIFICATION:

35 (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/087,009
(B) FILING DATE: 01-JUL-1993
(C) CLASSIFICATION:

40 (viii) ATTORNEY/AGENT INFORMATION:

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(C) REFERENCE/DOCKET NUMBER: UAG-004CP

45 (ix) TELECOMMUNICATION INFORMATION:

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50 (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
55 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

5 TATTAGTAGA TCTG 14

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

20 TACAGATGTA CTAA 14

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 846 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

35 (A) NAME/KEY: CDS
(B) LOCATION: 20..845

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

40 ACACAGCAAT CAGGTCAGC CAA AAT TAC CCT ATA GTG CAG AAC ATC CAG GGG 52
Gln Asn Tyr Pro Ile Val Gln Asn Ile Gln Gly
1 5 10

45 CAA ATG GTA CAT CAG GCC ATA TCA CCT AGA ACT TTA AAT GCA TGG GTA 100
Gln Met Val His Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val
15 20 25

50 AAA GTA GTA GAA GAG AAG GCT TTC AGC CCA GAA GTG ATA CCC ATG TTT 148
Lys Val Val Glu Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe
30 35 40

55 TCA GCA TTA TCA GAA GGA GCC ACC CCA CAA GAT TTA AAC ACC ATG CTA 196
Ser Ala Leu Ser Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu
45 50 55

	AAC	ACA	GTG	GGG	GGG	CAT	CAA	GCA	GCC	ATG	CAA	ATG	TTA	AAA	GAG	ACC	244
	Asn	Thr	Val	Gly	Gly	His	Gln	Ala	Ala	Met	Gln	Met	Leu	Lys	Glu	Thr	
	60					65					70					75	
5	ATC	AAT	GAG	GAA	GCT	GCA	GAA	TGG	GAT	AGA	GTG	CAT	CCA	GTG	CAT	GCA	292
	Ile	Asn	Glu	Glu	Ala	Ala	Glu	Trp	Asp	Arg	Val	His	Pro	Val	His	Ala	
					80					85					90		
10	GGG	CCT	ATT	GCA	CCA	GGC	CAG	ATG	AGA	GAA	CCA	AGG	GGA	AGT	GAC	ATA	340
	Gly	Pro	Ile	Ala	Pro	Gly	Gln	Met	Arg	Glu	Pro	Arg	Gly	Ser	Asp	Ile	
				95					100					105			
15	GCA	GGA	ACT	ACT	AGT	ACC	CTT	CAG	GAA	CAA	ATA	GGA	TGG	ATG	ACA	AAT	388
	Ala	Gly	Thr	Thr	Ser	Thr	Leu	Gln	Glu	Gln	Ile	Gly	Trp	Met	Thr	Asn	
			110					115					120				
20	AAT	CCA	CCT	ATC	CCA	GTA	GGA	GAA	ATT	TAT	AAA	AGA	TGG	ATA	ATC	CTG	436
	Asn	Pro	Pro	Ile	Pro	Val	Gly	Glu	Ile	Tyr	Lys	Arg	Trp	Ile	Ile	Leu	
		125					130					135					
25	GGA	TTA	AAT	AAA	ATA	GTA	AGA	ATG	TAT	AGC	CCT	ACC	AGC	ATT	CTG	GAC	484
	Gly	Leu	Asn	Lys	Ile	Val	Arg	Met	Tyr	Ser	Pro	Thr	Ser	Ile	Leu	Asp	
	140					145					150					155	
30	ATA	AGA	CAA	GGA	CCA	AAG	GAA	CCC	TTT	AGA	GAC	TAT	GTA	GAC	CGG	TTC	532
	Ile	Arg	Gln	Gly	Pro	Lys	Glu	Pro	Phe	Arg	Asp	Tyr	Val	Asp	Arg	Phe	
					160					165					170		
35	TAT	AAA	ACT	CTA	AGA	GCC	GAG	CAA	GCT	TCA	CAG	GAG	GTA	AAA	AAT	TGG	580
	Tyr	Lys	Thr	Leu	Arg	Ala	Glu	Gln	Ala	Ser	Gln	Glu	Val	Lys	Asn	Trp	
				175					180					185			
40	ATG	ACA	GAA	ACC	TTG	TTG	GTC	CAA	AAT	GCG	AAC	CCA	GAT	TGT	AAG	ACT	628
	Met	Thr	Glu	Thr	Leu	Leu	Val	Gln	Asn	Ala	Asn	Pro	Asp	Cys	Lys	Thr	
			190					195					200				
45	ATT	TTA	AAA	GCA	TTG	GGA	CCA	GCG	GCT	ACA	CTA	GAA	GAA	ATG	ATG	ACA	676
	Ile	Leu	Lys	Ala	Leu	Gly	Pro	Ala	Ala	Thr	Leu	Glu	Glu	Met	Met	Thr	
		205					210					215					
50	GCA	TGT	CAG	GGA	GTA	GGA	GGA	CCC	GGC	CAT	AAG	GCA	AGA	GTT	TTG	GCT	724
	Ala	Cys	Gln	Gly	Val	Gly	Gly	Pro	Gly	His	Lys	Ala	Arg	Val	Leu	Ala	
	220					225					230					235	
55	GAA	GCA	ATG	AGC	CAA	GTA	ACA	AAT	TCA	GCT	ACC	ATA	ATG	ATG	CAG	AGA	772
	Glu	Ala	Met	Ser	Gln	Val	Thr	Asn	Ser	Ala	Thr	Ile	Met	Met	Gln	Arg	
					240					245					250		
60	GGC	AAT	TTT	AGG	AAC	CAA	AGA	AAG	ATT	GTT	AAG	TGT	TTC	AAT	TGT	GGC	820
	Gly	Asn	Phe	Arg	Asn	Gln	Arg	Lys	Ile	Val	Lys						

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Gln Asn Tyr Pro Ile Val Gln Asn Ile Gln Gly Gln Met Val His Gln
1 5 10 15
Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val Glu Glu
20 25 30
Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser Glu
35 40 45
Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly Gly
50 55 60
His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu Glu Ala
65 70 75 80
Ala Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile Ala Pro
85 90 95
Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr Ser
100 105 110
Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro Ile Pro
115 120 125
Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys Ile
130 135 140
Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly Pro
145 150 155 160
Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu Arg
165 170 175
Ala Glu Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr Leu
180 185 190
Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala Leu
195 200 205
Gly Pro Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly Val
210 215 220
Gly Gly Pro Gly His Lys Ala Arg Val Leu Ala Glu Ala Met Ser Gln
225 230 235 240
Val Thr Asn Ser Ala Thr Ile Met Met Gln Arg Gly Asn Phe Arg Asn
245 250 255

Gln Arg Lys Ile Val Lys Cys Phe Asn Cys Gly Lys Glu Gly His Thr
260 265 270

5 Ala Arg Lys
275

(2) INFORMATION FOR SEQ ID NO:5:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 948 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

20 (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 4..946

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

25 AAC CAA TGG CCA TTG ACA GAA GAA AAA ATA AAA GCA TTA GTA GAA ATT 48
Gln Trp Pro Leu Thr Glu Glu Lys Ile Lys Ala Leu Val Glu Ile
1 5 10 15

30 TGT ACA GAG ATG GAA AAG GAA GGG AAA ATT TCA AAA ATT GGG CCT GAA 96
Cys Thr Glu Met Glu Lys Glu Gly Lys Ile Ser Lys Ile Gly Pro Glu
20 25 30

35 AAT CCA TAC AAT ACT CCA GTA TTT GCC ATA AAG AAA AAA GAC AGT ACT 144
Asn Pro Tyr Asn Thr Pro Val Phe Ala Ile Lys Lys Lys Asp Ser Thr
35 40 45

40 AAA TGG AGA AAA TTA GTA GAT TTC AGA GAA CTT AAT AAG AGA ACT CAA 192
Lys Trp Arg Lys Leu Val Asp Phe Arg Glu Leu Asn Lys Arg Thr Gln
50 55 60

GAC TTC TGG GAA GTT CAA TTA GGA ATA CCA CAT CCC GCA GGG TTA AAA 240
Asp Phe Trp Glu Val Gln Leu Gly Ile Pro His Pro Ala Gly Leu Lys
65 70 75

45 AAG AAA AAA TCA GTA ACA GTA CTG GAT GTG GGT GAT GCA TAT TTT TCA 288
Lys Lys Lys Ser Val Thr Val Leu Asp Val Gly Asp Ala Tyr Phe Ser
80 85 90 95

50 GTT CCC TTA GAT GAA GAC TTC AGG AAG TAT ACT GCA TTT ACC ATA CCT 336
Val Pro Leu Asp Glu Asp Phe Arg Lys Tyr Thr Ala Phe Thr Ile Pro
100 105 110

55 AGT ATA AAC AAT GAG ACA CCA GGG ATT AGA TAT CAG TAC AAT GTG CTT 384
Ser Ile Asn Asn Glu Thr Pro Gly Ile Arg Tyr Gln Tyr Asn Val Leu
115 120 125



CCA CAG GGA TGG AAA GGA TCA CCA GCA ATA TTC CAA AGT AGC ATG ACA 432
Pro Gln Gly Trp Lys Gly Ser Pro Ala Ile Phe Gln Ser Ser Met Thr
130 135 140

5 AAA ATC TTA GAG CCT TTT AGA AAA CAA AAT CCA GAC ATA GTT ATC TAT 480
Lys Ile Leu Glu Pro Phe Arg Lys Gln Asn Pro Asp Ile Val Ile Tyr
145 150 155

10 CAA TAC ATG GAT GAT TTG TAT GTA GGA TCT GAC TTA GAA ATA GGG CAG 528
Gln Tyr Met Asp Asp Leu Tyr Val Gly Ser Asp Leu Glu Ile Gly Gln
160 165 170 175

15 CAT AGA ACA AAA ATA GAG GAG CTG AGA CAA CAT CTG TTG AGG TGG GGA 576
His Arg Thr Lys Ile Glu Glu Leu Arg Gln His Leu Leu Arg Trp Gly
180 185 190

CTT ACC ACA CCA GAC AAA AAA CAT CAG AAA GAA CCT CCA TTC CTT TGG 624
Leu Thr Thr Pro Asp Lys Lys His Gln Lys Glu Pro Pro Phe Leu Trp
195 200 205

20 ATG GGT TAT GAA CTC CAT CCT GAT AAA TGG ACA GTA CAG CCT ATA GTG 672
Met Gly Tyr Glu Leu His Pro Asp Lys Trp Thr Val Gln Pro Ile Val
210 215 220

25 CTG CCA GAA AAA GAC AGC TGG ACT GTC AAT GAC ATA CAG AAG TTA GTG 720
Leu Pro Glu Lys Asp Ser Trp Thr Val Asn Asp Ile Gln Lys Leu Val
225 230 235

30 GGG AAA TTG AAT TGG GCA AGT CAG ATT TAC CCA GGG ATT AAA GTA AGG 768
Gly Lys Leu Asn Trp Ala Ser Gln Ile Tyr Pro Gly Ile Lys Val Arg
240 245 250 255

35 CAA TTA TGT AAA CTC CTT AGA GGA ACC AAA GCA CTA ACA GAA GTA ATA 816
Gln Leu Cys Lys Leu Leu Arg Gly Thr Lys Ala Leu Thr Glu Val Ile
260 265 270

40 CCA CTA ACA GAA GAA GCA GAG CTA GAA CTG GCA GAA AAC AGA GAG ATT 864
Pro Leu Thr Glu Glu Ala Glu Leu Glu Leu Ala Glu Asn Arg Glu Ile
275 280 285

CTA AAA GAA CCA GTA CAT GGA GTG TAT TAT GAC CCA TCA AAA GAC TTA 912
Leu Lys Glu Pro Val His Gly Val Tyr Tyr Asp Pro Ser Lys Asp Leu
290 295 300

45 ATA GCA GAA ATA CAG AAG CAG GGG CAA GGC CTCGAG 948
Ile Ala Glu Ile Gln Lys Gln Gly Gln Gly
305 310

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(2) INFORMATION FOR SEQ ID NO:6:

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- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 314 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

5 Gln Trp Pro Leu Thr Glu Glu Lys Ile Lys Ala Leu Val Glu Ile Cys
1 5 10 15
Thr Glu Met Glu Lys Glu Gly Lys Ile Ser Lys Ile Gly Pro Glu Asn
20 25 30
10 Pro Tyr Asn Thr Pro Val Phe Ala Ile Lys Lys Lys Asp Ser Thr Lys
35 40 45
Trp Arg Lys Leu Val Asp Phe Arg Glu Leu Asn Lys Arg Thr Gln Asp
50 55 60
15 Phe Trp Glu Val Gln Leu Gly Ile Pro His Pro Ala Gly Leu Lys Lys
65 70 75 80
Lys Lys Ser Val Thr Val Leu Asp Val Gly Asp Ala Tyr Phe Ser Val
85 90 95
20 Pro Leu Asp Glu Asp Phe Arg Lys Tyr Thr Ala Phe Thr Ile Pro Ser
100 105 110
25 Ile Asn Asn Glu Thr Pro Gly Ile Arg Tyr Gln Tyr Asn Val Leu Pro
115 120 125
Gln Gly Trp Lys Gly Ser Pro Ala Ile Phe Gln Ser Ser Met Thr Lys
130 135 140
30 Ile Leu Glu Pro Phe Arg Lys Gln Asn Pro Asp Ile Val Ile Tyr Gln
145 150 155 160
Tyr Met Asp Asp Leu Tyr Val Gly Ser Asp Leu Glu Ile Gly Gln His
165 170 175
35 Arg Thr Lys Ile Glu Glu Leu Arg Gln His Leu Leu Arg Trp Gly Leu
180 185 190
40 Thr Thr Pro Asp Lys Lys His Gln Lys Glu Pro Pro Phe Leu Trp Met
195 200 205
Gly Tyr Glu Leu His Pro Asp Lys Trp Thr Val Gln Pro Ile Val Leu
210 215 220
45 Pro Glu Lys Asp Ser Trp Thr Val Asn Asp Ile Gln Lys Leu Val Gly
225 230 235 240
Lys Leu Asn Trp Ala Ser Gln Ile Tyr Pro Gly Ile Lys Val Arg Gln
245 250 255
50 Leu Cys Lys Leu Leu Arg Gly Thr Lys Ala Leu Thr Glu Val Ile Pro
260 265 270
Leu Thr Glu Glu Ala Glu Leu Glu Leu Ala Glu Asn Arg Glu Ile Leu
275 280 285

Lys Glu Pro Val His Gly Val Tyr Tyr Asp Pro Ser Lys Asp Leu Ile
 290 295 300

5 Ala Glu Ile Gln Lys Gln Gly Gln Gly Leu
 305 310

(2) INFORMATION FOR SEQ ID NO:7:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1568 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: cDNA

20 (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 7..1565

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

25	GGGGCC TGT CCA AAG GTA TCC TTT GAG CCA ATT CCC ATA CAT TAT TGT Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys 1 5 10	48
30	GCC CCG GCT GGT TTT GCG ATT CTA AAA TGT AAT AAT AAG ACG TTC AAT Ala Pro Ala Gly Phe Ala Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn 15 20 25 30	96
35	GGA ACA GGA CCA TGT ACA AAT GTC AGC ACA GTA CAA TGT ACA CAT GGA Gly Thr Gly Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His Gly 35 40 45	144
40	ATT AGG CCA GTA GTA TCA ACT CAA CTG CTG TTA AAT GGC AGT CTA GCA Ile Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala 50 55 60	192
45	GAA GAA GAG GTA GTA ATT AGA TCT GTC AAT TTC ACG GAC AAT GCT AAA Glu Glu Glu Val Val Ile Arg Ser Val Asn Phe Thr Asp Asn Ala Lys 65 70 75	240
50	ACC ATA ATA GTA CAG CTG AAC ACA TCT GTA GAA ATT AAT TGT ACA AGA Thr Ile Ile Val Gln Leu Asn Thr Ser Val Glu Ile Asn Cys Thr Arg 80 85 90	288
55	CCC AAC AAC AAT ACA AGA AAA AGA ATC CGT ATC CAG AGA GGA CCA GGG Pro Asn Asn Asn Thr Arg Lys Arg Ile Arg Ile Gln Arg Gly Pro Gly 95 100 105 110	336
	AGA GCA TTT GTT ACA ATA GGA AAA ATA GGA AAT ATG AGA CAA GCA CAT Arg Ala Phe Val Thr Ile Gly Lys Ile Gly Asn Met Arg Gln Ala His 115 120 125	384

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TTG CTG AGG GCT ATT GAG GCG CAA CAG CAT CTG TTG CAA CTC ACA GTC	1104
Leu Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val	
355 360 365	
TGG GGC ATC AAG CAG CTC CAA GCA AGA ATC CTA GCT GTG GAA AGA TAC	1152
Trp Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu Arg Tyr	
370 375 380	
CTA AAG GAT CAA CAG CTC CTA GGG ATT TGG GGT TGC TCT GGA AAA CTC	1200
Leu Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu	
385 390 395	
ATT TGC ACC ACT GCT GTG CCT TGG AAT GCT AGT TGG AGT AAT AAA TCT	1248
Ile Cys Thr Thr Ala Val Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser	
400 405 410	
CTG GAA CAG ATC TGG AAT CAC ACG ACC TGG ATG GAG TGG GAC AGA GAA	1296
Leu Glu Gln Ile Trp Asn His Thr Thr Trp Met Glu Trp Asp Arg Glu	
415 420 425 430	
ATT AAC AAT TAC ACA AGC TTA ATA CAC TCC TTA ATT GAA GAA TCG CAA	1344
Ile Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln	
435 440 445	
AAC CAG CAA GAA AAG AAT GAA CAA GAA TTA TTG GAA TTA GAT AAA TGG	1392
Asn Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp	
450 455 460	
GCA AGT TTG TGG AAT TGG TTT AAC ATA ACA AAT TGG CTG TGG TAT ATA	1440
Ala Ser Leu Trp Asn Trp Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile	
465 470 475	
AAA TTA TTC ATA ATG ATA GTA GGA GGC TTG GTA GGT TTA AGA ATA GTT	1488
Lys Leu Phe Ile Met Ile Val Gly Gly Leu Val Gly Leu Arg Ile Val	
480 485 490	
TTT GCT GTA CTT TCT ATA GTG AAT AGA GTT AGG CAG GGA TAT TCA CCA	1536
Phe Ala Val Leu Ser Ile Val Asn Arg Val Arg Gln Gly Tyr Ser Pro	
495 500 505 510	
TTA TCG TTT CAG ACC CAC CTC CCA ATC TCGAG	1568
Leu Ser Phe Gln Thr His Leu Pro Ile	
515	

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 519 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

5 Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro
1 5 10 15

Ala Gly Phe Ala Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly Thr
20 25 30

10 Gly Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg
35 40 45

Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu
50 55 60

15 Glu Val Val Ile Arg Ser Val Asn Phe Thr Asp Asn Ala Lys Thr Ile
65 70 75 80

20 Ile Val Gln Leu Asn Thr Ser Val Glu Ile Asn Cys Thr Arg Pro Asn
85 90 95

Asn Asn Thr Arg Lys Arg Ile Arg Ile Gln Arg Gly Pro Gly Arg Ala
100 105 110

25 Phe Val Thr Ile Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys Asn
115 120 125

Ile Ser Arg Ala Lys Trp Asn Asn Thr Leu Lys Gln Ile Asp Ser Lys
130 135 140

30 Leu Arg Glu Gln Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys Gln Ser
145 150 155 160

35 Ser Gly Gly Asp Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly Gly
165 170 175

Glu Phe Phe Tyr Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp Phe
180 185 190

40 Asn Ser Thr Trp Ser Thr Glu Gly Ser Asn Asn Thr Glu Gly Ser Asp
195 200 205

Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn Met Trp Gln
210 215 220

45 Lys Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile Arg
225 230 235 240

50 Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly Asn
245 250 255

Ser Asn Asn Glu Ser Glu Ile Phe Arg Leu Gly Gly Gly Asp Met Arg
260 265 270

55 Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile Glu
275 280 285

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[illegible]

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(2) INFORMATION FOR SEQ ID NO:9:

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(B) TYPE: nucleic acid

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CACCCCTCTC CTACGTAACC AAGGATC

27

5 (2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: cDNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GTACTGGTCA CCATATTGGT CAAC

24

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(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: cDNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGAGAGAGAT GGGAGCTCGA GCGTC

25

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(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

40

(ii) MOLECULE TYPE: cDNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GCCCCCTAT ACGTATTGTG

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(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CCAGTGAATT CCTAATACGA CTCACTATAG GTTAAACAG C

41

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(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 48 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: cDNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CTCTATCCTG AGCTCCATAT GTGTCGAGCA GTTTTGGTT TAGCATTG

48

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(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: peptide

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(v) FRAGMENT TYPE: internal

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Thr Lys Asp Leu Thr Thr Tyr Gly
1 5

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(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2220 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: cDNA

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(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..2203

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

5	CGA CCA GCA GAC CAG ACA GTC ACA GCA GCC TTG ACA AAA CGT TCC TGG	48
	Arg Pro Ala Asp Gln Thr Val Thr Ala Ala Leu Thr Lys Arg Ser Trp	
	1 5 10 15	
10	AAC TCA AGC ACT TCT CCA CAG AGG AGG ACA GAG CAG ACA GCA GAG ACC	96
	Asn Ser Ser Thr Ser Pro Gln Arg Arg Thr Glu Gln Thr Ala Glu Thr	
	20 25 30	
15	ATG GAG TCT CCC TCG GCC CCT CCC CAC AGA TGG TGC ATC CCC TGG CAG	144
	Met Glu Ser Pro Ser Ala Pro Pro His Arg Trp Cys Ile Pro Trp Gln	
	35 40 45	
20	AGG CTC CTG CTC ACA GCC TCA CTT CTA ACC TTC TGG AAC CCG CCC ACC	192
	Arg Leu Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn Pro Pro Thr	
	50 55 60	
25	ACT GCC AAG CTC ACT ATT GAA TCC ACG CCG TTC AAT GTC GCA GAG GGG	240
	Thr Ala Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val Ala Glu Gly	
	65 70 75 80	
30	AAG GAG GTG CTT CTA CTT GTC CAC AAT CTG CCC CAG CAT CTT TTT GGC	288
	Lys Glu Val Leu Leu Val His Asn Leu Pro Gln His Leu Phe Gly	
	85 90 95	
35	TAC AGC TGG TAC AAA GGT GAA AGA GTG GAT GGC AAC CGT CAA ATT ATA	336
	Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Ile	
	100 105 110	
40	GGA TAT GTA ATA GGA ACT CAA CAA GCT ACC CCA GGG CCC GCA TAC AGT	384
	Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Tyr Ser	
	115 120 125	
45	GGT CGA GAG ATA ATA TAC CCC AAT GCA TCC CTG CTG ATC CAG AAC ATC	432
	Gly Arg Glu Ile Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Ile	
	130 135 140	
50	ATC CAG AAT GAC ACA GGA TTC TAC ACC CTA CAC GTC ATA AAG TCA GAT	480
	Ile Gln Asn Asp Thr Gly Phe Tyr Thr Leu His Val Ile Lys Ser Asp	
	145 150 155 160	
55	CTT GTG AAT GAA GAA GCA ACT GGC CAG TTC CGG GTA TAC CCG GAG CTG	528
	Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu	
	165 170 175	
60	CCC AAG CCC TCC ATC TCC AGC AAC AAC TCC AAA CCC GTG GAG GAC AAG	576
	Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro Val Glu Asp Lys	
	180 185 190	
65	GAT GCT GTG GCC TTC ACC TGT GAA CCT GAG ACT CAG GAC GCA ACC TAC	624
	Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp Ala Thr Tyr	
	195 200 205	
70	CTG TGG TGG GTA AAC AAT CAG AGC CTC CCG GTC AGT CCC AGG CTG CAG	672
	Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Gln	

	210	215	220	
5	CTG TCC AAT GGC AAC AGG ACC CTC ACT CTA TTC AAT GTC ACA AGA AAT Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn Val Thr Arg Asn 225 230 235 240	720		
10	GAC ACA GCA AGC TAC AAA TGT GAA ACC CAG AAC CCA GTG AGT GCC AGG Asp Thr Ala Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Ala Arg 245 250 255	768		
15	CGC AGT GAT TCA GTC ATC CTG AAT GTC CTC TAT GGC CCG GAT GCC CCC Arg Ser Asp Ser Val Ile Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro 260 265 270	816		
20	ACC ATT TCC CCT CTA AAC ACA TCT TAC AGA TCA GGG GAA AAT CTG AAC Thr Ile Ser Pro Leu Asn Thr Ser Tyr Arg Ser Gly Glu Asn Leu Asn 275 280 285	864		
25	CTC TCC TGC CAT GCA GCC TCT AAC CCA CCT GCA CAG TAC TCT TGG TTT Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Phe 290 295 300	912		
30	GTC AAT GGG ACT TTC CAG CAA TCC ACC CAA GAG CTC TTT ATC CCC AAC Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn 305 310 315 320	960		
35	ATC ACT GTG AAT AAT AGT GGA TCC TAT ACG TGC CAA GCC CAT AAC TCA Ile Thr Val Asn Asn Ser Gly Ser Tyr Thr Cys Gln Ala His Asn Ser 325 330 335	1008		
40	GAC ACT GGC CTC AAT AGG ACC ACA GTC ACG ACG ATC ACA GTC TAT GCA Asp Thr Gly Leu Asn Arg Thr Thr Val Thr Thr Ile Thr Val Tyr Ala 340 345 350	1056		
45	GAG CCA CCC AAA CCC TTC ATC ACC AGC AAC AAC TCC AAC CCC GTG GAG Glu Pro Pro Lys Pro Phe Ile Thr Ser Asn Asn Ser Asn Pro Val Glu 355 360 365	1104		
50	GAT GAG GAT GCT GTA GCC TTA ACC TGT GAA CCT GAG ATT CAG AAC ACA Asp Glu Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Ile Gln Asn Thr 370 375 380	1152		
55	ACC TAC CTG TGG TGG GTA AAT AAT CAG AGC CTC CCG GTC AGT CCC AGG Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg 385 390 395 400	1200		
60	CTG CAG CTG TCC AAT GAC AAC AGG ACC CTC ACT CTA CTC AGT GTC ACA Leu Gln Leu Ser Asn Asp Asn Arg Thr Leu Thr Leu Leu Ser Val Thr 405 410 415	1248		
65	AGG AAT GAT GTA GGA CCC TAT GAG TGT GGA ATC CAG AAC GAA TTA AGT Arg Asn Asp Val Gly Pro Tyr Glu Cys Gly Ile Gln Asn Glu Leu Ser 420 425 430	1296		
70	GTT GAC CAC AGC GAC CCA GTC ATC CTG AAT GTC CTC TAT GGC CCA GAC Val Asp His Ser Asp Pro Val Ile Leu Asn Val Leu Tyr Gly Pro Asp 435 440 445	1344		

TTT ATC GCC AAA ATC ACG CCA AAT AAT AAC GGG ACC TAT GCC TGT TTT 2064
Phe Ile Ala Lys Ile Thr Pro Asn Asn Asn Gly Thr Tyr Ala Cys Phe
675 680 685

5 GTC TCT AAC TTG GCT ACT GGC CGC AAT AAT TCC ATA GTC AAG AGC ATC 2112
Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Ser Ile
690 695 700

10 ACA GTC TCT GCA TCT GGA ACT TCT CCT GGT CTC TCA GCT GGG GCC ACT 2160
Thr Val Ser Ala Ser Gly Thr Ser Pro Gly Leu Ser Ala Gly Ala Thr
705 710 715 720

15 GTC GGC ATC ATG ATT GGA GTG CTG GTT GGG GTT GCT CTG ATA 2202
Val Gly Ile Met Ile Gly Val Leu Val Gly Val Ala Leu Ile
725 730

TAGCAGCCCT GGTGTAGT 2220

20 (2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 734 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Arg Pro Ala Asp Gln Thr Val Thr Ala Ala Leu Thr Lys Arg Ser Trp
1 5 10 15

Asn Ser Ser Thr Ser Pro Gln Arg Arg Thr Glu Gln Thr Ala Glu Thr
20 25 30

Met Glu Ser Pro Ser Ala Pro Pro His Arg Trp Cys Ile Pro Trp Gln
35 40 45

Arg Leu Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn Pro Pro Thr
50 55 60

Thr Ala Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val Ala Glu Gly
65 70 75 80

Lys Glu Val Leu Leu Leu Val His Asn Leu Pro Gln His Leu Phe Gly
85 90 95

Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Ile
100 105 110

Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Tyr Ser
115 120 125

Gly Arg Glu Ile Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Ile
130 135 140

	Ile	Gln	Asn	Asp	Thr	Gly	Phe	Tyr	Thr	Leu	His	Val	Ile	Lys	Ser	Asp	
	145					150					155					160	
5	Leu	Val	Asn	Glu	Glu	Ala	Thr	Gly	Gln	Phe	Arg	Val	Tyr	Pro	Glu	Leu	
					165				170						175		
	Pro	Lys	Pro	Ser	Ile	Ser	Ser	Asn	Asn	Ser	Lys	Pro	Val	Glu	Asp	Lys	
				180					185						190		
10	Asp	Ala	Val	Ala	Phe	Thr	Cys	Glu	Pro	Glu	Thr	Gln	Asp	Ala	Thr	Tyr	
			195					200					205				
	Leu	Trp	Trp	Val	Asn	Asn	Gln	Ser	Leu	Pro	Val	Ser	Pro	Arg	Leu	Gln	
		210					215					220					
15	Leu	Ser	Asn	Gly	Asn	Arg	Thr	Leu	Thr	Leu	Phe	Asn	Val	Thr	Arg	Asn	
	225					230					235					240	
	Asp	Thr	Ala	Ser	Tyr	Lys	Cys	Glu	Thr	Gln	Asn	Pro	Val	Ser	Ala	Arg	
20					245					250					255		
	Arg	Ser	Asp	Ser	Val	Ile	Leu	Asn	Val	Leu	Tyr	Gly	Pro	Asp	Ala	Pro	
				260					265					270			
25	Thr	Ile	Ser	Pro	Leu	Asn	Thr	Ser	Tyr	Arg	Ser	Gly	Glu	Asn	Leu	Asn	
			275					280					285				
	Leu	Ser	Cys	His	Ala	Ala	Ser	Asn	Pro	Pro	Ala	Gln	Tyr	Ser	Trp	Phe	
		290					295					300					
30	Val	Asn	Gly	Thr	Phe	Gln	Gln	Ser	Thr	Gln	Glu	Leu	Phe	Ile	Pro	Asn	
	305					310					315					320	
	Ile	Thr	Val	Asn	Asn	Ser	Gly	Ser	Tyr	Thr	Cys	Gln	Ala	His	Asn	Ser	
35				325						330					335		
	Asp	Thr	Gly	Leu	Asn	Arg	Thr	Thr	Val	Thr	Thr	Ile	Thr	Val	Tyr	Ala	
				340					345					350			
40	Glu	Pro	Pro	Lys	Pro	Phe	Ile	Thr	Ser	Asn	Asn	Ser	Asn	Pro	Val	Glu	
			355					360					365				
	Asp	Glu	Asp	Ala	Val	Ala	Leu	Thr	Cys	Glu	Pro	Glu	Ile	Gln	Asn	Thr	
45							375					380					
	Thr	Tyr	Leu	Trp	Trp	Val	Asn	Asn	Gln	Ser	Leu	Pro	Val	Ser	Pro	Arg	
	385					390					395					400	
	Leu	Gln	Leu	Ser	Asn	Asp	Asn	Arg	Thr	Leu	Thr	Leu	Leu	Ser	Val	Thr	
50					405					410					415		
	Arg	Asn	Asp	Val	Gly	Pro	Tyr	Glu	Cys	Gly	Ile	Gln	Asn	Glu	Leu	Ser	
				420					425					430			
55	Val	Asp	His	Ser	Asp	Pro	Val	Ile	Leu	Asn	Val	Leu	Tyr	Gly	Pro	Asp	
			435					440					445				

Asp Pro Thr Ile Ser Pro Ser Tyr Thr Tyr Tyr Arg Pro Gly Val Asn
 450 455 460
 5 Leu Ser Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser
 465 470 475 480
 Trp Leu Ile Asp Gly Asn Ile Gln Gln His Thr Gln Glu Leu Phe Ile
 485 490 495
 10 Ser Asn Ile Thr Glu Lys Asn Ser Gly Leu Tyr Thr Cys Gln Ala Asn
 500 505 510
 Asn Ser Ala Ser Gly His Ser Arg Thr Thr Val Lys Thr Ile Thr Val
 515 520 525
 15 Ser Ala Glu Leu Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro
 530 535 540
 20 Val Glu Asp Lys Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Ala Gln
 545 550 555 560
 Asn Thr Thr Tyr Leu Trp Trp Val Asn Gly Gln Ser Leu Pro Val Ser
 565 570 575
 25 Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn
 580 585 590
 Val Thr Arg Asn Asp Ala Arg Ala Tyr Val Cys Gly Ile Gln Asn Ser
 595 600 605
 30 Val Ser Ala Asn Arg Ser Asp Pro Val Thr Leu Asp Val Leu Tyr Gly
 610 615 620
 35 Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Ser Ser Tyr Leu Ser Gly
 625 630 635 640
 Ala Asn Leu Asn Leu Ser Cys His Ser Ala Ser Asn Pro Ser Pro Gln
 645 650 655
 40 Tyr Ser Trp Arg Ile Asn Gly Ile Pro Gln Gln His Thr Gln Val Leu
 660 665 670
 Phe Ile Ala Lys Ile Thr Pro Asn Asn Asn Gly Thr Tyr Ala Cys Phe
 675 680 685
 45 Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Ser Ile
 690 695 700
 50 Thr Val Ser Ala Ser Gly Thr Ser Pro Gly Leu Ser Ala Gly Ala Thr
 705 710 715 720
 Val Gly Ile Met Ile Gly Val Leu Val Gly Val Ala Leu Ile
 725 730

55 (2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 41 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

10 CCAGTGAATT CCTAATACGA CTACCTATAG GTTAAAACAG C

41

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

25 GATGAACCCT CGAGACCCAT TATG

24

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

40 CCACCAAGTA CGTAACCACA TATGG

25

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

55 GTGAGGACTG CTGG

14

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

15 CACCACTGCC CTCGAGAAGC TCACTATTG

29

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

30 CACCACTGCC CTCGAGAAGC TCACTATTG

29